



IFWO

RAW SEQUENCE LISTING

DATE: 08/06/2004

PATENT APPLICATION: US/10/807,807A

TIME: 11:12:55

Input Set : D:\V9661077.app

Output Set: N:\CRF4\08062004\J807807A.raw

3 <110> APPLICANT: LEUNG, FREDERICK C.
 4 PEIRIS, JOSEPH S. M.
 5 YUEN, KWOK YUNG
 6 POON, LIT MAN
 7 GUAN, YI
 8 CHAN, KWOK HUNG
 9 NICHOLLS, JOHN M.
 11 <120> TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
 12 CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
 14 <130> FILE REFERENCE: V9661.0077
 16 <140> CURRENT APPLICATION NUMBER: 10/807,807A
 17 <141> CURRENT FILING DATE: 2004-03-24
 19 <150> PRIOR APPLICATION NUMBER: 60/457,031
 20 <151> PRIOR FILING DATE: 2003-03-24
 22 <150> PRIOR APPLICATION NUMBER: 60/457,730
 23 <151> PRIOR FILING DATE: 2003-03-26
 25 <150> PRIOR APPLICATION NUMBER: 60/459,931
 26 <151> PRIOR FILING DATE: 2003-04-02
 28 <150> PRIOR APPLICATION NUMBER: 60/460,357
 29 <151> PRIOR FILING DATE: 2003-04-03
 31 <150> PRIOR APPLICATION NUMBER: 60/461,265
 32 <151> PRIOR FILING DATE: 2003-04-08
 34 <150> PRIOR APPLICATION NUMBER: 60/462,805
 35 <151> PRIOR FILING DATE: 2003-04-14
 37 <150> PRIOR APPLICATION NUMBER: 60/464,886
 38 <151> PRIOR FILING DATE: 2003-04-23
 40 <150> PRIOR APPLICATION NUMBER: 60/465,738
 41 <151> PRIOR FILING DATE: 2003-04-25
 43 <150> PRIOR APPLICATION NUMBER: 60/470,935
 44 <151> PRIOR FILING DATE: 2003-05-14
 46 <160> NUMBER OF SEQ ID NOS: 2487
 48 <170> SOFTWARE: PatentIn ver. 3.2
 50 <210> SEQ ID NO: 1
 51 <211> LENGTH: 646
 52 <212> TYPE: DNA
 53 <213> ORGANISM: Human severe acute respiratory syndrome virus
 55 <220> FEATURE:
 56 <221> NAME/KEY: CDS
 57 <222> LOCATION: (2)...(646)
 59 <400> SEQUENCE: 1
 60 a cag gac gct gta gct tca aaa atc tta gga ttg cct acg cag act gtt 49
 61 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
 62 1 5 10 15

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64 gat tca tca cag ggt tct gaa tat gac tat gtc ata ttc aca caa act 97
65 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
66          20          25          30
68 act gaa aca gca cac tct tgt aat gtc aac cgc ttc aat gtg gct atc 145
69 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile
70          35          40          45
72 aca agg gca aaa att ggc att ttg tgc ata atg tct gat aga gat ctt 193
73 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
74          50          55          60
76 tat gac aaa ctg caa ttt aca agt cta gaa ata cca cgt cgc aat gtg 241
77 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
78          65          70          75          80
80 gct aca tta caa gca gaa aat gta act gga ctt ttt aag gac tgt agt 289
81 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
82          85          90          95
84 aag atc att act ggt ctt cat cct aca cag gca cct aca cac ctc agc 337
85 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
86          100          105          110
88 gtt gat ata aaa ttc aag act gaa gga tta tgt gtt gac ata cca ggc 385
89 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
90          115          120          125
92 ata cca aag gac atg acc tac cgt aga ctc atc tct atg atg ggt ttc 433
93 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
94          130          135          140
96 aaa atg aat tac caa gtc aat ggt tac cct aat atg ttt atc acc cgc 481
97 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
98          145          150          155          160
100 gaa gaa gct att cgt cac gtt cgt gcg tgg att ggc ttt gat gta gag 529
101 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
102          165          170          175
104 ggc tgt cat gca act aga gat gct gtg ggt act aac cta cct ctc cag 577
105 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
106          180          185          190
108 cta gga ttt tct aca ggt gtt aac tta gta gct gta ccg act ggt tat 625
109 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
110          195          200          205
112 gtt gac act gaa aat aac cta 646
113 Val Asp Thr Glu Asn Asn Leu
114          210          215
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 215
119 <212> TYPE: PRT
120 <213> ORGANISM: Human severe acute respiratory syndrome virus
122 <400> SEQUENCE: 2
123 Gln Asp Ala Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val
124 1          5          10          15
126 Asp Ser Ser Gln Gly Ser Glu Tyr Asp Tyr Val Ile Phe Thr Gln Thr
127          20          25          30
129 Thr Glu Thr Ala His Ser Cys Asn Val Asn Arg Phe Asn Val Ala Ile

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130          35          40          45
132 Thr Arg Ala Lys Ile Gly Ile Leu Cys Ile Met Ser Asp Arg Asp Leu
133          50          55          60
135 Tyr Asp Lys Leu Gln Phe Thr Ser Leu Glu Ile Pro Arg Arg Asn Val
136 65          70          75          80
138 Ala Thr Leu Gln Ala Glu Asn Val Thr Gly Leu Phe Lys Asp Cys Ser
139          85          90          95
141 Lys Ile Ile Thr Gly Leu His Pro Thr Gln Ala Pro Thr His Leu Ser
142          100          105          110
144 Val Asp Ile Lys Phe Lys Thr Glu Gly Leu Cys Val Asp Ile Pro Gly
145          115          120          125
147 Ile Pro Lys Asp Met Thr Tyr Arg Arg Leu Ile Ser Met Met Gly Phe
148          130          135          140
150 Lys Met Asn Tyr Gln Val Asn Gly Tyr Pro Asn Met Phe Ile Thr Arg
151 145          150          155          160
153 Glu Glu Ala Ile Arg His Val Arg Ala Trp Ile Gly Phe Asp Val Glu
154          165          170          175
156 Gly Cys His Ala Thr Arg Asp Ala Val Gly Thr Asn Leu Pro Leu Gln
157          180          185          190
159 Leu Gly Phe Ser Thr Gly Val Asn Leu Val Ala Val Pro Thr Gly Tyr
160          195          200          205
162 Val Asp Thr Glu Asn Asn Leu
163          210          215
166 <210> SEQ ID NO: 3
167 <211> LENGTH: 17
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
173     nucleotide sequence of the genome of hSARS
175 <400> SEQUENCE: 3
176 tacacacctc agcggttg                                     17
178 <210> SEQ ID NO: 4
179 <211> LENGTH: 16
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: primer sequence for RT-PCT based on partial
185     nucleotide sequence of the genome of hSARS
187 <400> SEQUENCE: 4
188 cacgaacgtg acgaat                                     16
190 <210> SEQ ID NO: 5
191 <211> LENGTH: 27
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <223> OTHER INFORMATION: degenerated primer in Superscript II Kit by
197     Invitrogen
199 <220> FEATURE:

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200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (21)..(27)
202 <223> OTHER INFORMATION: a, t, c or g
204 <400> SEQUENCE: 5
W--> 205 gccggagctc tgcagaattc nnnnnnnn                27
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 20
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: primer provided in AmpliTaq Gold Kit by Applied
214     Biosyndromes
216 <400> SEQUENCE: 6
217 gccggagctc tgcagaattc                20
219 <210> SEQ ID NO: 7
220 <211> LENGTH: 17
221 <212> TYPE: DNA
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: First round of primer for amplifying human
226     metapneumovirus (HMPV)
228 <400> SEQUENCE: 7
229 aargtsaatg catcagc                17
231 <210> SEQ ID NO: 8
232 <211> LENGTH: 20
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: first round primer for amplifying human
238     metapneumovirus (HMPV)
240 <400> SEQUENCE: 8
241 cakattytgc ttatgctttc                20
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 20
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
248 <220> FEATURE:
249 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
250     (HMPV)
252 <400> SEQUENCE: 9
253 acacctgtta caataccagc                20
255 <210> SEQ ID NO: 10
256 <211> LENGTH: 19
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: nested primer for amplifying human metapneumovirus
262     (HMPV)
264 <400> SEQUENCE: 10

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Input Set : D:\V9661077.app

Output Set: N:\CRF4\08062004\J807807A.raw

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265 gacttgagtc ccagctcca                                19
267 <210> SEQ ID NO: 11
268 <211> LENGTH: 1213
269 <212> TYPE: DNA
270 <213> ORGANISM: Human severe acute respiratory syndrome virus
272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (2)...(1213)
276 <400> SEQUENCE: 11
277 t aaa tgt agt aga atc ata cct gcg cgt gcg cgc gta gag tgt ttt gat 49
278   Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala Arg Val Glu Cys Phe Asp
279     1           5           10           15
281 aaa ttc aaa gtg aat tca aca cta gaa cag tat gtt ttc tgc act gta 97
282   Lys Phe Lys Val Asn Ser Thr Leu Glu Gln Tyr Val Phe Cys Thr Val
283     20           25           30
285 aat gca ttg cca gaa aca act gct gac att gta gtc ttt gat gaa atc 145
286   Asn Ala Leu Pro Glu Thr Thr Ala Asp Ile Val Val Phe Asp Glu Ile
287     35           40           45
289 tct atg gct act aat tat gac ttg agt gtt gtc aat gct aga ctt cgt 193
290   Ser Met Ala Thr Asn Tyr Asp Leu Ser Val Val Asn Ala Arg Leu Arg
291     50           55           60
293 gca aaa cac tac gtc tat att ggc gat cct gct caa tta cca gcc ccc 241
294   Ala Lys His Tyr Val Tyr Ile Gly Asp Pro Ala Gln Leu Pro Ala Pro
295     65           70           75           80
297 cgc aca ttg ctg act aaa ggc aca cta gaa cca gaa tat ttt aat tca 289
298   Arg Thr Leu Leu Thr Lys Gly Thr Leu Glu Pro Glu Tyr Phe Asn Ser
299     85           90           95
301 gtg tgc aga ctt atg aaa aca ata ggt cca gac atg ttc ctt gga act 337
302   Val Cys Arg Leu Met Lys Thr Ile Gly Pro Asp Met Phe Leu Gly Thr
303     100          105          110
305 tgt cgc cgt tgt cct gct gaa att gtt gac act gtg agt gct tta gtt 385
306   Cys Arg Arg Cys Pro Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val
307     115          120          125
309 tat gac aat aag cta aaa gca cac aag gag aag tca gct caa tgc ttc 433
310   Tyr Asp Asn Lys Leu Lys Ala His Lys Glu Lys Ser Ala Gln Cys Phe
311     130          135          140
313 aaa atg ttc tac aaa ggt gtt att aca cat gat gtt tca tct gca atc 481
314   Lys Met Phe Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile
315     145          150          155          160
317 aac aga cct caa ata ggc gtt gta aga gaa ttt ctt aca cgc aat cct 529
318   Asn Arg Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn Pro
319     165          170          175
321 gct tgg aga aaa gct gtt ttt atc tca cct tat aat tca cag aac gct 577
322   Ala Trp Arg Lys Ala Val Phe Ile Ser Pro Tyr Asn Ser Gln Asn Ala
323     180          185          190
325 gta gct tca aaa atc tta gga ttg cct acg cag act gtt gat tca tca 625
326   Val Ala Ser Lys Ile Leu Gly Leu Pro Thr Gln Thr Val Asp Ser Ser
327     195          200          205
329 cag ggt tct gaa tat gac tat gtc ata ttc aca caa act act gaa aca 673

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/06/2004
PATENT APPLICATION: US/10/807,807A TIME: 11:12:56

Input Set : D:\V9661077.app
Output Set: N:\CRF4\08062004\J807807A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 21,22,23,24,25,26,27

VERIFICATION SUMMARY

DATE: 08/06/2004

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TIME: 11:12:56

Input Set : D:\V9661077.app

Output Set: N:\CRF4\08062004\J807807A.raw

L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0